*FY*
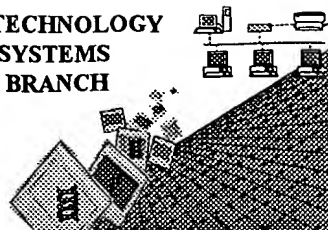
# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/673,994_
Source: _PCT/09_
Date Processed by STIC: _2/13/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/673,994 |

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)          SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT09

```
RAW SEQUENCE LISTING              DATE: 02/13/2002
PATENT APPLICATION:  US/09/673,994      TIME: 07:45:38

        Input Set : A:\B08017197.txt
        Output Set: N:\CRF3\02132002\I673994.raw
```

**Does Not Comply**
**Corrected Diskette Needed**

*ツァ 1-2, 4-6*

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  3 <110> APPLICANT: Chen, Yuqing E.
  4         Tamura, Koichi
  5         Horiuchi, Masatsugu
  6         Dzau, Victor J.
  8 <120> TITLE OF INVENTION: CNRE Binding Factors and Uses Thereof
 10 <130> FILE REFERENCE: B0801/7197/ERG/KA
 12 <140> CURRENT APPLICATION NUMBER: US 09/673994
 13 <141> CURRENT FILING DATE: 2000-10-24
 15 <150> PRIOR APPLICATION NUMBER: US 60/082,997
 16 <151> PRIOR FILING DATE: 1998-04-24
 18 <150> PRIOR APPLICATION NUMBER: PCT/US99/08502
 19 <151> PRIOR FILING DATE: 1999-04-23
 21 <160> NUMBER OF SEQ ID NOS: 23
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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ERRORED SEQUENCES

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    310 <213> ORGANISM: Mus musculus
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E--> 315     aaacaganaa ttttttttga gatgtgagca gaggttggga gttagattca ctgaanacaa     180
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*ツァ 1-2*

*) see*
*) item 9*
*on Error*
*Summary*
*Sheet*

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        343   ttaaaggaac  ctgagggtca  tcgagtacgg  gaagtgcagt  tcacaacagc  tggctccttg   1860
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RAW SEQUENCE LISTING                DATE: 02/13/2002
PATENT APPLICATION:  US/09/673,994        TIME: 07:45:38

Input Set : A:\B08017197.txt
Output Set: N:\CRF3\02132002\I673994.raw

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388             20                  25                  30
389 Val Met Leu Arg Leu Arg Ser Gly Cys Thr Ala His Glu Leu Arg Ile
390         35                  40                  45
391 Pro Cys Cys Ser Ala Val Ala Glu Ala Glu Ala Gly Thr Glu Val Pro
392     50                  55                  60
393 Ala Gly Leu Arg Arg Gly Val Gly Gly Ser Met Asn Gly Ser Gly Gly
394 65                  70                  75                  80
395 Gly Gly Gly Ser Asp Leu Ser Trp Ile Pro Gly Pro Gly Gln Gly Leu
396             85                  90                  95
397 Pro Arg Ala Arg Thr Val Tyr Gly Gly Gly Ser Trp Ile Leu Arg Ala
398             100                 105                 110
399 Arg Thr Asp Gly Arg Ala Glu Leu Gly Gly Ala Gly Pro Gly Gly Leu
400         115                 120                 125
401 Gly Pro Glu Ala Arg Arg Ala Gly Ala Gly His Asp Ala Pro Lys Glu
402         130                 135                 140
403 Ala Lys Pro Ser Thr Ala Arg Glu Met Arg Gly Gly Gln Arg Ser Gly
404 145                 150                 155                 160
405 Val Arg Gly Leu Glu Pro Gly Gly Thr Gly Val Gly Ser Val Glu Trp
406             165                 170                 175
407 Ala Gln Val Arg Val Glu Gly Asp Ser Ser Gly Leu Gly Ala Asp Asp
408             180                 185                 190
409 Leu Gly Ser Ser Leu Leu Thr Arg Val Leu Lys Glu Pro Glu Gly His
410         195                 200                 205
411 Arg Val Arg Glu Val Gln Phe Thr Thr Ala Gly Ser Leu Val Arg Ile
412     210                 215                 220
413 Met Gly Thr Ala Trp Glu Gly Asp Ser Thr Ser Thr Leu Pro Ser Leu
414 225             230                 235                 240
415 Val Asp Thr Glu Asp Ser Phe Asp Glu Gly Pro Gly Ala Leu Val Leu
416             245                 250                 255
417 Glu Ser Asp Leu Leu Leu Gly Gln Asp Leu Glu Phe Glu Glu Glu Glu
418             260                 265                 270
419 Glu Glu Asp Glu Gly Asp Gly His Asn Asp Gln Leu Met Gly Phe Glu
420         275                 280                 285
421 Arg Asp Ser Glu Gly Asp Ser Gln Gly Ala Arg Pro Gly Leu Pro Tyr
422     290                 295                 300
423 Gly Leu Ser Asp Asp Glu Ser Gly Gly Gly Arg Ala Leu Ser Ala Glu
424 305             310                 315                 320
425 Ser Glu Val Glu Glu Pro Ala Arg Gly Pro Gly Glu Ala Arg Gly Glu
426             325                 330                 335
427 Arg Pro Gly Pro Ala Cys Gln Leu Cys Gly Gly Pro Thr Gly Glu Gly
428         340                 345                 350
429 Pro Cys Cys Gly Ala Gly Gly Arg Gly Gly Gly Pro Pro Leu Pro Pro
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431 Arg Leu Leu Tyr Ser Cys Arg Leu Cys Ala Phe Val Ser His Tyr Ser
432     370                 375                 380
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Input Set : A:\B08017197.txt
Output Set: N:\CRF3\02132002\I673994.raw

*see → item 9*

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436                       405             410                 415
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440               435             440                 445
441   Thr His Thr Gly Pro Pro Thr Pro Pro Cys Pro Thr Cys Gly Phe Arg
442       450             455             460
443   Cys Cys Ala Pro Arg Pro Thr Arg Pro Pro Ser Pro Thr Glu Gln Glu
444   465             470             475                 480
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446               485             490             495
447   Ser Leu His Val Pro Pro Gly Gly Ala Ser Phe Leu Pro Asp Cys Gly
448               500             505             510
449   Gln Leu Arg Gly Glu Gly Glu Ser Leu Cys Gly Thr Gly Ser Glu Pro
450               515             520             525
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454   545             550             555                 560
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458               580             585             590
459   Tyr Pro Asn His Leu Ala Arg His Met Lys Thr His Ser Gly Glu Lys
460               595             600             605
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462       610             615             620
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465   Pro Leu Cys Pro Tyr Ala Cys Gly Asn Leu Ala Asn Leu Lys Arg His
466               645             650             655
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468               660             665             670
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474   705             710             715                 720
475   Ala Gly Gly Pro Gly Leu Ser Ala Pro Glu Gly Trp Ala Pro Pro His
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     514  ttgtgtggaa  ctggatccga  accactgcca  gagctactgt  tcccttggac  ctgccggggc    1620
     515  tgtggacagg  aactggagga  gggtgagggc  agcaggctgg  gagctgccat  gtgtgggcgc    1680
     516  tgcatgcgag  gagaggctgg  aggggttgcc ·actgggggac  cccagggccc  tggtgacaaa    1740
     517  ggctttgcct  gtagtttatg  cccctttgcc  actcactacc  ccaaccacct  ggctcggcac    1800
     518  atgaagactc  acagtggtga  gaaacccttc  cgctgtgccc  gctgtccata  cgcctctgct    1860
     519  catctggata  acctgaaacg  gcaccagcgc  gtccacacag  gagaaaagcc  ctacaagtgc    1920
     520  cccctctgtc  cgtatgcctg  tggcaacctg  gccaacctca  agcgtcatgg  tcgcatccac    1980
     521  tctggtgaca  aaccttttcg  gtgtagcctt  tgcaactaca  gctgcaacca  gagtatgaac    2040
     522  ctcaaacgtc  atatgctgcg  acacacgggc  gagaagccct  tccgctgtgc  cacctgcgcc    2100
     523  tataccacag  gccactggga  caactacaag  cgtcatcaga  aggtgcatgg  ccatggtgga    2160
     524  gcaggagggc  ctggtctctc  tgcccctgag  ggctgggccc  cacctcatag  cccaccctct    2220
     525  gttttgagca  ctcggggtcc  agcagccctg  ggtgctactg  gtagcagggc  tcttcattca    2280
     526  gactcacct                                                               2289
     606 <210> SEQ ID NO: 15
     607 <211> LENGTH: 581
     608 <212> TYPE: DNA
     609 <213> ORGANISM: Mus musculus
     611 <400> SEQUENCE: 15
     612  ggcctttagt  ctgaaaaagt  gttgcttgaa  agtgtacaac  agagagcggg  tgcaagcggc      60
```

E--> (handwritten) item 9

(handwritten) p. 6

```
        613  taggggtcac agagccgcca ataaaaaaga atgtccttaa ataaagtgtt cacagagtaa        120
        614  aaatcagaac taccagtcct tccctccaac acaacagagc acaggcacag aaccgatagt        180
        615  cgatgagccc aaggagagta aggaggctta agaggacagc agagcctccc aggctgccgc        240
        616  gtgggggggg tgggggggccc tctttgtaat gggctgagga aagccacca gccccctgca         300
        617  cacctcatac ccactgctaa ggctaaagga caaggacaaa actcagtctc gggtccaagg        360
        618  gctcagaaaa cagtccacat gggcagggtc cggttgacca ctagtccctc ttggccttct        420
        619  ttttgtcact gttgccggtg tcttcagccc cctccgtgga cagtgcctcc tccagtttcc        480
E--> 620  tcttgccant ctctgcctga agctctactg tgtttcgggg cttgaagcaa atgatgatgc        540
        621  acgtcatgtt gtcacaccct gtaccatccc cagaagtgtc t                          581
        623  <210> SEQ ID NO: 16
        624  <211> LENGTH: 586
        625  <212> TYPE: DNA
        626  <213> ORGANISM: Mus musculus
        628  <400> SEQUENCE: 16
        629  gcttttgttt ggcctttagt ctgaaaaagt gttgcttgaa agtgtacaac agagagcggg         60
        630  tgcaagcggc taggggtcac agagccgcca ataaaaaaga atgtccttaa ataaagtgtt        120
        631  cacagagtaa aaatcagaac taccagtcct tccctccaac acaacagagc acaggcacag        180
        632  aaccgatagt cgatgagccc aaggagagta aggaggctta agaggacagc agagcctccc        240
        633  aggctgccgc gtgggggggg tggggggccc tctttgtaat gggctgagga aagccaccca        300
        634  gccccctgca cacctcatac ccactgctaa ggctaaagga caaggacaaa actcagtctc        360
        635  gggtccaagg ggctcagaaa aacagttcca catggggcag ggtccggttg aaccactagt        420
        636  tccctcttgg gccttctttt tgttcactgt tggccggtgt cttcagcccc ctccgtggac        480
E--> 637  agtgcctcct ccagtttcct cttgccactc ttctgnctga agtctactgt gtttcggggn        540
        638  tgaagcaaat gatgatgcac ttcatgttgt tcacaccctg taccat                      586
```

*Item 9* (handwritten, next to line 620)

*Item 9* (handwritten, next to line 637)

VERIFICATION SUMMARY                    DATE: 02/13/2002
PATENT APPLICATION:   US/09/673,994     TIME: 07:45:39

        Input Set : A:\B08017197.txt
        Output Set: N:\CRF3\02132002\I673994.raw

L:314 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:435 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:508 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:620 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:637 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16